

Figure 1A

1 TCGAACTCAC TCACCTCCCC TCTCACCTCA CTGCCCTCAC CAGCCAGCCT
 51 CTTGTCAAGT GATCAGGCTG TCAACCAACT TCTCTAGGAT AAGGTTTCAG
 101 GTCAGCCTGT GTGTATAAGA CCAGTGCCAA GCCAGAAGCA GCAGAGACAA
 151 CAGTGAATGA CAAGGAGGGG CCATCCAATC CCTGCTGCCA CCTCCTGGGA
 201 TGGAGCCCTA GGGAGCCCCCT GTGCTGCCCC TGCCGTGGCA GGACTCACAG
 251 CCCCACCGCT GCACTGAAGC CCAGGGCTGT GGAGCAGCTC TCTCCTTGGA
 301 CTCCTCTCGG CCTTAAAGGG ACTGGGCAGA GCCTTCCAGG ACTATGGTTG
 351 GACTGAAGCC TTCAGACGTG CCTCCCACCA TGGCTGTGAA GTTCCTGGGG
 401 GCAGGCACAG CAGCCTGTTT TGCTGACCTC GTTACCTTTC CACTGGACAC
 451 AGCCAAGGTC CGCCTGCAGA TCCAGGGGGA GAACCAGGCG GTCCAGACGG
 501 CCGGGCTCGT GCASTACCGT GCGGTGCTGG GCACCATCCT GACCATGGTG
 551 CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CCGGCCTGCA
 601 GCGCCAGATG AGCTTCGCTT CCATCCGCAT CGGCCTTTAC GACTCCGTCA
 651 AGCAGGTGTA CACCCCCAAA GCGCGGGA CACTCCAGCCT CACTACCCGG
 701 ATTTTGGCCG GCTGCACCAC AGGAGCCATG GCGGTGACCT GTGCCCAGCC
 751 CACAGATGTG GTGAAGGTCC GATTTCAGGC CAGCATACAC CTCGGGCCAT
 801 CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA CAGAACCATC
 851 GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAACTT TGCCCAACAT
 901 CATGAGGAAT GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACGACATCC
 951 TCAAGGAGAA GCTGCTGGAC TATCACCTGC TCACTGACAA CTTCCTCTGC
 1001 CACTTTGTCT CTGCCCTTGG AGCCGGCTTC TGTGCCACAG TGGTGGCCTC
 1051 CCGGTGGAC GTGGTGAAGA CCGGTATAT GAACTCCTT CCAGGCCAGT
 1101 ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA GGAGGGCCCC
 1151 ACAGCCTTCT ACAAGGGATT TACACCTCC TTTTTCGCTT TGGGATCCTG
 1201 GAACGTGGTG ATGTTCTGTA CCTATGAGCA GCTGAAACGG GCCCTGATGA
 1251 AAGTCCAGAT GTTACGGGA TCACCGTTTT GAACAAGACA AGAAGGCCAC
 1301 TGGTAGCTAA CGTGTCCGAA ACCAGTTAAG AATGGAAGAA AACGGTGCAT

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1351 CCACGCACAC ATGGACACAG ACCCACACAT GTTTACAGAA CTGTTGTTTA
1401 CTTGTTGCTG ATTCAAGAAA CAGAAGTAGA AGAGAGAGGA TTCTGGTCTT
1451 CACTGCCATG CCTCAAGAAC ACCTTTGTTT TGCAC TGACA AGATGGAAAA
1501 TAAATTATAT TAATTTTTGA AACCATTAG GCATGCCTAA TATTTAGGCA
1551 AGAGAAAATA AACCAAGATA GATCCATTG GACAAAATGG AAGGTTGGAG
1601 ACGTGTATCC CCGTGAAATC TGGTCAGATA ATGAATGATA AGCAGGAAGG
1651 ATGGCAAGCA CGGGACAGGA GGGGCCCCACA ATGGAGTGGG AGATCAGCCA
1701 CGGAGCCTGG AGGGACGCCA CCCAGCAACA CAGAGCTGGC GACTGCAGCT
1751 GCACCATCAC ACATGCATCA TCAGCCTATT TGTAATATGT CTGCCACAGA
1801 GAGTCCTTTG GGATTCTAGG AAACCCAAGG AACAAAGAGAA AAAACTAGAG
1851 CCTGTGCTAA AGAAGCCTGC TGGGCCCCATG TGAGGCTGGG GTCGTAAATA
1901 TTCCCCGACG ACACTGAAGA ATCAAGAGGG CAGCCCCCAC TTCTCCTACA
1951 AAATGGAGGG AGCCATCCCT TCCCTGTCCA CCTCACCAGG GGTGCTATGA
2001 CATGCAAGTG AGAAGCTGGG CATGAACGCA CTTTATAAAA GCAAAGCTC
2051 TGTGTAAATC TAACTACAAG GACAATGCCT TGGGAGAGAT TTTGTGGGA
2101 CAGAGAGGAG TTGCCAGGGA AGAAGGTTTG AAAGATACGG TTGTCTAGAG
2151 GTGAGACCAA AGGATCCAGA GACTTGGGGA CCAGAGGTGA CAGTGGATGA
2201 CGTGAAGCCA CAGGAGCCCC ACCCCCATGC AGCTTTTTTC CCACCCCCC
2251 CACCACGCGC TCAATCATGA GTACCTCAA GGATTGTTGG GCTTGGGGGA
2301 AAAGAGGTGG ATTCTGGGC AAGAACCTAA AGTAGCAGGA (Seq ID NO. 11)

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1	AGCTTGAGTGAGTGGAGGGGAGAGTGGAGTGACGGGAGTGGTGGTGGGAGAACAGTTCA	60
	GATCAGGCTGTCAACCAACTTCTCTAGGATAAGGTTTCAGGTCAGCCTGTGTGTATAAGA	
61	CTAGTCCGACAGTTGGTTGAAGAGATCCTATTCCAAAGTCCAGTCGGACACACATATTCT	120
	CCAGTGCCAAGGCCAGAAGCAGCAGAGACAACAGTGAATGACAAGGAGGGGCCATCCAATC	
121	GGTTCACGGTTCCGGTCTTCGTCTCTGTGTCACTTACTGTTCCTCCCCGGTAGGTTAG	180
	CCTGCTGCCACCTCTCTGGGATGGAGCCCTAGGGAGCCCTGTGCTGCCCTGCCGTGGCA	
181	GGACGACGGTGGAGGACCTTACCTCGGGATCCCTCGGGGACACGACGGGGACGGCACCGT	240
	GGACTCACAGCCCCACCGCTGCACTGAAGGCCAGGGCTGTGGAGCAGCTCTCTCCTTGA	
241	CCTGAGTGTCTGGGGTGGCGACGTGACTTCGGGTCTCCGACACCTCGTTCGAGAGAGGAACCT	300
	CTCCTCTCGGCCCCCTAAAGGGACTGGGCAGAGCCTTCCAGGACTATGGTTGGACTGAAGCC	
301	GAGGAGAGCCCGGATTTCCCTGACCCGCTCTCGGAAGGTCTGATACCAACCTGACTTCGG	360
	M V G L K P	
	TTGAGACGTGCCTCCCACCATGGCTGTGAAGTTCTTGGGGGAGGCACAGCAGCCTGTTT	
361	AAGTCTGCACGGAGGGTGGTACCGACACTTCAAGGACCCCGTCCGTGTCTGTCGGACAAA	420
	S D V P P T M A V K F L G A G T A A C F	
	TGCTGACCTCGTTACCTTTCCACTGGACACAGCCAAAGGTCCGCTTCAGATCCAGGGGA	
421	ACGACTGGAGCAATGGAAAAGGTGACCTGTGTCTGGTTCCAGGCGGACGTCTAGGTCCCCCT	480
	A D L V T F P L D T A K V R L Q I Q G E	
	GAACCAGGCGGTCCAGACGGCCCCGGCTCGTGCAGTACCGTGGCGTGTGGGCACCATCCT	
481	CTTGGTCCGCCAGGTCTGCCGGGCGGACACGTGATGGCACCCGACGACCCGTGGTAGGA	540
	N Q A V Q T A R L V Q Y R G V L G T I L	
	GACCATGGTGGCAGTGAAGGTCCCTGCAGCCCCCTACAAAGGGCTGGTGGCCGGCCTGCA	
541	CTGGTACCACGCTGACTCCAGGGACGTGGGGATGTTACCCGACCACCGCCGGGACGT	600
	T M V R T E G P C S P Y N G L V A G L Q	
	BCGCCAGATGAGCTTCGCTCCATCCGCACTCGGCTTTACGACTCCGTCAAGCAGGTGTA	
601	CGCGGTCTACTCGAAGCGGAGGTAGGCGTAGCCGGAATGCTGAGGCAGTTCTGCCACAT	660
	R Q M S F A S I R I G L Y D S V K Q V Y	
	CACCCCCAAAGGCCCGGACAACTCCAGCCTCACTACCCGATTTTGGCCCGCTGCACCAC	
661	GTGGGGGTTTCCCGGCTGTGAGGTCCGAGTGATGGGCTTAAACCGGCGGACGTGGTG	720
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[illegible]

Figure 2C

1381 GTTTACAGAACTGTTGTTTACTTGTGCTGATTCAAGAAAAGAGAGAGAGGA 1440

 CAAAATGCTCTTGACAACAAATGAACAACGACTAAGTTCTTTGTCTTCATCTTCTCTCTCT
 1441 TTCTGGTCTTCACTGCCATGCCCTCAAGAACACCTTTGTTTTGCACTGACAAGATGGAAA 1500

 AAGACCAGAAAGTGACGGTACGGAGTTCTTGTGGAAAACAAAACGTGACTGTTCTACCTTTT
 1501 TAAATTATATTAATTTTTGAAACCCATTAGGCATGCCCTAATATTTAGGCAAGAGAAAAATA 1560

 ATTTAATATAATTAATAAACTTTGGGTAATCCGTACGGATTATAAATCCGTTCTCTTTTAT
 1561 AACCAAGATAGATCCATTTGGACAAAAATGGAAGGTTGGAGACGTGTATCCCCGTGAAATC 1620

 TTGGTTCTATCTAGGTAACCTGTTTTACCTTCCAACCTCTGCACATAGGGGCACCTTTAG
 1621 TGGTCAGATAATGAATGATAAGCAGGAAGGATGGCAAGCACGGGACAGGAGGGGGCCACA 1680

 ACCAGTCTATTACTTACTATTGTCCTTCTTACCGTTGCTGCCCTGTCTCTCCCGGGTGT
 1681 ATGGAGTGGGAGATCAGCCACGGAGCCTGGAGGGACGCCACCCAGCAACACAGAGCTGGC 1740

 TACCTCACCTCTAGTCTGGTGCCTCGGACCTCCCTGCGGTGGGTCTGTGTCTCGACCG
 1741 GACTGCAGCTGCACCATCACACATGCATCATCAGCCTATTTGTAATATGTCTGCCACAGA 1800

 CTGACGTGACGTGGTAGTGTGTACGTAGTAGTGGATAAACATTATACAGACGGTGTCT
 1801 GAGTCCTTTGGGATTCTAGGAAACCCAAGGAACAAGAGAAAAAACTAGAGCCTGTGCTAA 1860

 CTCAGGAAACCTAAGATCCTTTGGGTTCTTGTCTCTTTTTTGATCTCGGACACGATT
 1861 AGAAGCCTGCTGGGCCCCATGTGAGGCTGGGGTCTGTAATATTTCCCCGACGACACTGAAGA 1920

 TCTTCGGACGACCCGGGTACACTCGGACCCCGCATTTATAAGGGGCTGCTGTGACTTCT
 1921 ATCAAGAGGGGACGCCCCCACTTCTCTACAAAAATGGAGGGAGCCATCCCTTCCCTGTCCA 1980

 TAGTTCTCCCGTCCGGGTGAAGAGGATGTTTTACCTCCCTCGGTAGGGAAGGGACAGGT
 1981 CCTCACCAGGGGTGCTATGACATGCAAGTGAGAGCTGGGCAAGCACTTTATAAAA 2040

 GGAGTGGTCCCCACGATACTGTACGTTCACTCTTCGACCCGTACTTGGGTGAAATATTTT
 2041 GCAAAAGCTCTGTGTAATCTAACTACAAGGACAAATGCCCTGGGAGAGATTTTGTGGGA 2100

 CGTTTTGAGACACATTTAGATTGATGTTCTCTTACGGAACTCTCTATAAACAGCCCT
 2101 CAGAGAGGAGTTGCCAGGGAAGAAGGTTTGAAGATACGTTGTCTAGAGGTGAGACCAA 2160

 GTCTCTCTCAACGGTCCCTTCTTCCAACTTTCTATGCCAACAGATCTCCACTCTGGTT
 AGGATCCAGAGACTTGGGACCAAGAGGTGACAGTGGATGACGTGAAGCCACAGGAGCCCC

00047-05190

[illegible]

Figure 3

1 MVGLKPSDVP PTMAVKFLGA GTAACFADLV TFPLDTAKVR LQIQGENQAV
51 QTARLVQYRG VLGITILTMVR TEGPCSPYNG LVAGLQRQMS FASIRIGLYD
101 SVKQVYTPKG ADNSSLTTRI LAGCTTGAMA VTCAOPTDVV KVRFAQSIHL
151 GPSRSDRKYS GTMDAYRTIA REEGVRGLWK GTLPNIMRNA IVNCAEVVTY
201 DILKEKLLDY HLLTDNFPCH FVSAPGAGFC ATVVASFVDV VKTRYMNSPP
251 GQYFSPIDCM IKMVAQEGPT AFYKGFTPSF LRLGSWNVVM FVTYEQLKRA
301 LMKVQMLRES PF* (SEQ ID NO: 12)

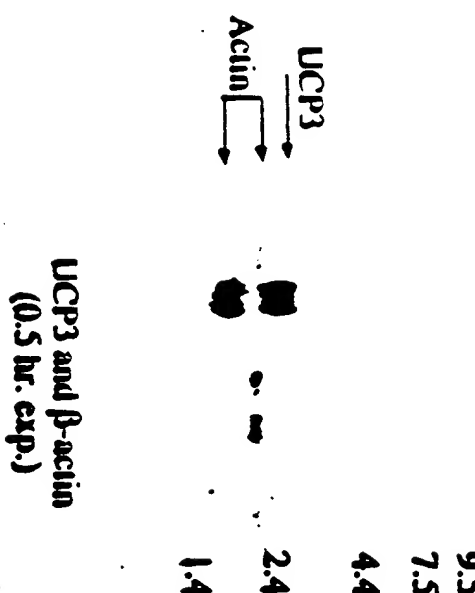
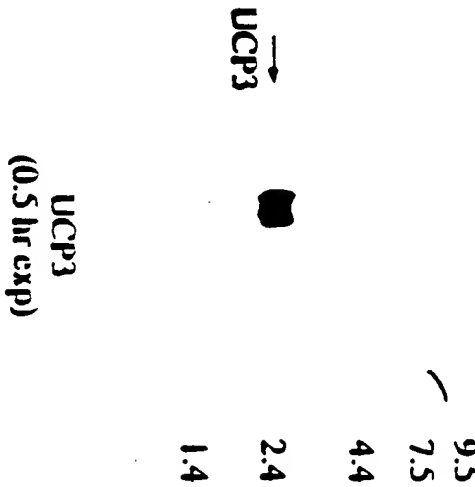
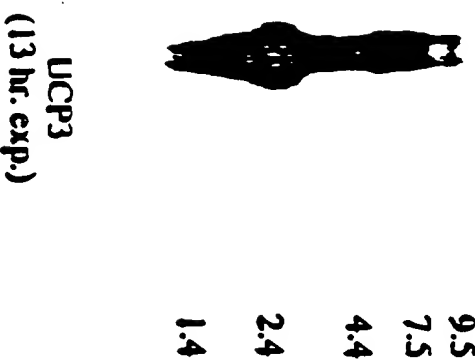
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Northern Analysis of UCP3 Expression in Human Tissues

- Pancreas
 - Kidney
 - Skeletal Muscle
 - Liver
 - Lung
 - Placenta
 - Brain
 - Heart
- MW(kb)

- Pancreas
 - Kidney
 - Skeletal Muscle
 - Liver
 - Lung
 - Placenta
 - Brain
 - Heart
- MW(kb)

- Pancreas
 - Kidney
 - Skeletal Muscle
 - Liver
 - Lung
 - Placenta
 - Brain
 - Heart
- MW(kb)



4A

4B

4C

3' EST
AA192E53

5' EST
AA192136

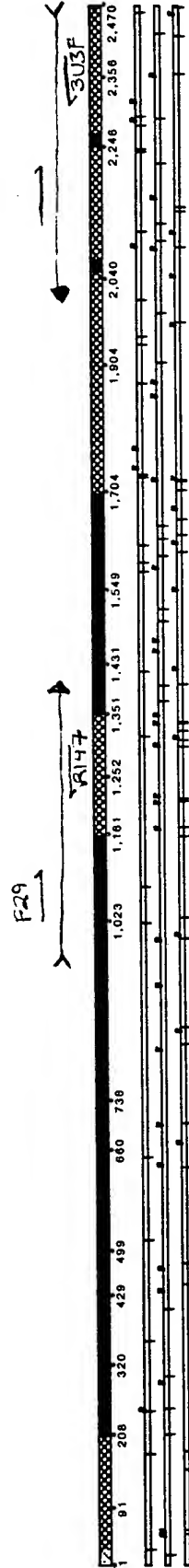


Diagram Key	
	Hole in contig
	Single fragment
	Multiple fragments same direction
	Both strands
	Both strands plus
	Start codon frame 1
	Stop codon frame 2
	Bumps on fragments
	show motifs
	hollow
	rectangles
	show features

1 CCAGGAACAG CAGAGACAAC AGTGAATGGT GAGGCCCGGC CGTCAGATCC
51 TGCTGCTACC TAATGGAGTG GATCCTTAGG GTGGCCCTGC ACTACCCAAC
101 CTTGGCTAGA CGCACAGCTT CCTCCCTGAA CTGAAGCAAA AGATTGCCAG
151 GCAAGCTCTC TCCTCGGACC TCCATAGGCA GCAAAGGAAC CAGGCCCATT
201 CCCCCGGGACC ATGGTTGGAC TTCAGCCCTC CGAAGTGCCT CCCACAACGG
251 TTGTGAAGTT CCTGGGGGCC GGCACGCGG CCTGTTTTGC GGACCTCCTC
301 ACTTTTCCCC TGGACACCGC CAAGGTCCGT CTGCAGATCC AAGGGGAGAA
351 CCCAGGGGCT CAGAGCGTGC AGTACCGCGG TGTGCTGGGT ACCATCCTGA
401 CTATGGTGCG CACAGAGGGT CCCCCGAGCC CCTACAGCGG ACTGGTCGCT
451 GGCCTGCACC GCCAGATGAG TTTTGCCTCC ATTGGAATTG GCCTCTACGA
501 CTCTGTCAAG CAGTTCTACA CCCCCAAGGG AGCGGACCAC TCCAGCGTCG
551 CCATCAGGAT TCTGGCAGGC TGCACGACAG GAGCCATGGC AGTGACCTGC
601 GCCCAGCCCA CGGATGTGGT GAAGGTCCGA TTTCAAGCCA TGATACGCCT
651 GGGAACTGGA GGAGAGAGGA AATACAGAGG GACTATGGAT GCCTACAGAA
701 CCATCGCCAG GGAGGAAGGA GTCAGGGGCC TGTGGAAAGG GACTTGGCCC
751 AACATCACAA GAAATGCCAT TGTCAACTGT GCTGAGATGG TGACCTACGA
801 CATCATCAAG GAGAAGTTGC TGGAGTCTCA CCTGTTTACT GACAACTTCC
851 CCTGTCACTT TGTCTCTGCC TTTGGAGCTG GCTTCTGTGC CACAGTGGTG
901 GCCTCCCCGG TGGATGTGGT AAAGACCCGA TACATGAACG CTCCCCTAGG
951 CAGGTACCGC AGCCCTCTGC ACTGTATGCT GAAGATGGTG GCTCAGGAGG

FIGURE 6A

1001 GACCCACGGC CTTCTACAAA GGATTTGTGC CCTCCTTTCT GCGTCTGGGA
1051 GCTTGGAACG TGATGATGTT TGTAACATAT GAGCAACTGA AGAGGGCCTT
1101 AATGAAAGTC CAGGTACTGC GGAATCTCC GTTTTGAACA AGGCAAGCAG
1151 GCTGCCTGGA ACAGAACAAA GCGTCTCTGC CCTGGGGACA CAGGCCCCACA
1201 CGGTCCAGAA CCCTGCACTG CTGCTGACAC GAGAACTGA ACTAAAAGAG
1251 GAGAGTTTTA GTCCTCCGTG TTTCGTCCTA AAACACCTCT GTTTTGCCT
1301 GACCTGATGG GAAATAAATT ATATTAATTT TTAAACCCTT TCCGGTTGGA
1351 TGCCTAACAT TTAGGCAAGA GACAACAAAG AAAACCAGAG TCAACTCCCT
1401 TGAAATGTAG GAATAAGGA TGCATAATAA ACAGGAAAGG CACAGGTTTT
1451 GAGAAGATCA GCCCACAGTG TTGTCCTTGA ATCAAACAAA ATGGTCGGAG
1501 GAACCCTTCG GGTTTCAGCAC AAAGAGGTGA CTACAGCCTT TTGGTCACCA
1551 GATGACTCCG CCCCTTTGTA ATGAGTCTGC CAAGTAGACT CTATCAAGAT
1601 TCTGGGGAAA GGAGAAAGAA CACATTGACC TGCCCGGGCG GCCGCTCGAG
1651 CCCTATGA (SEQ ID NO:17)

FIGURE 6B

1 MVGLQPSEVP PTTVVKFLGA GTAACFADLL TFPLDTAKVR LQIQGENPGA
51 QSVQYRGVLG TILTMVRTEG PRSPYSGLVA GLHRQMSFAS IRIGLYDSVK
101 QFYTPKGADH SSVAIRILAG CTTGAMAVTC AQPTDVVKVR FQAMIRLGTG
151 GERKYRGTMD AYRTIAREEG VRGLWKGTWP NITRNAIVNC AEMVTYDIIK
201 EKLLESHLFT DNFPCHFVSA FGAGFCATVV ASPVDVVKTR YMNAPLGGRYR
251 SPLHCMLKMV AQEGPTAFYK GFVPSFLRLG AWWMMFVTY EQLKRALMKV
301 QVLRESPF* (SEQ ID NO:18)

FIGURE 7

05013-0509

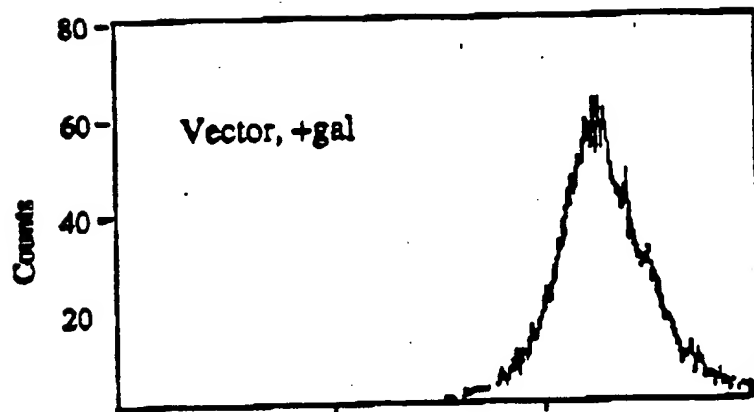


FIGURE 8A

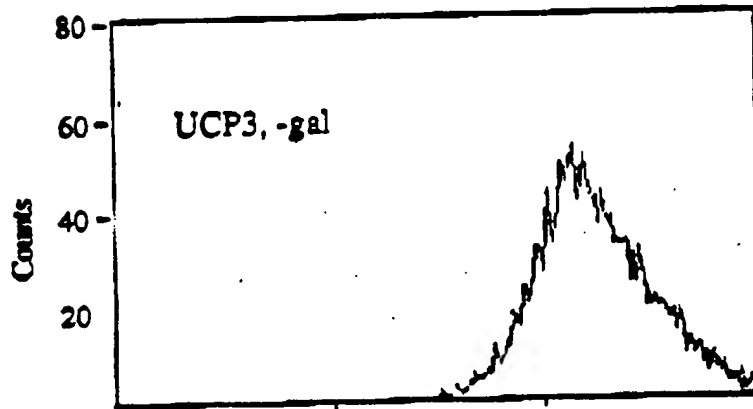


FIGURE 8B

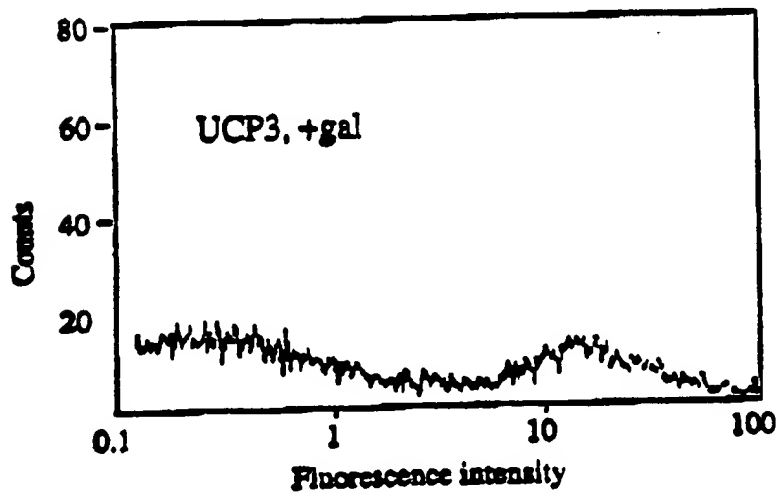


FIGURE 8C

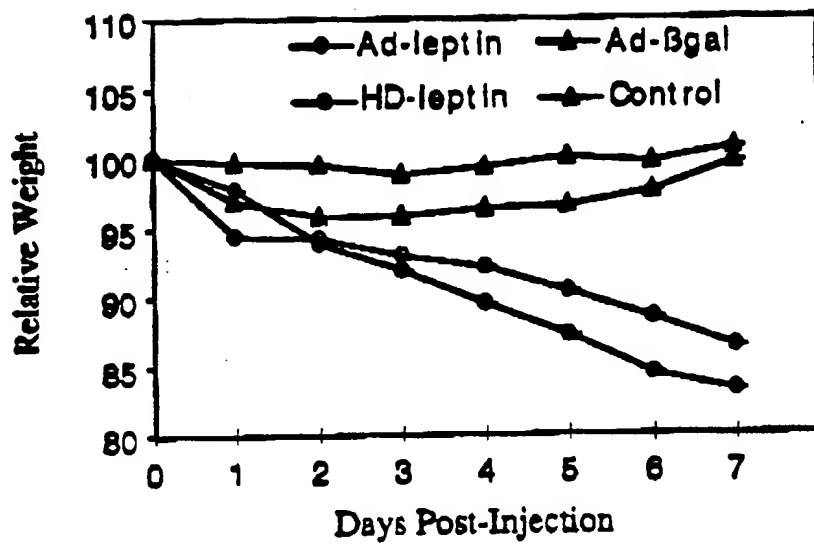


FIGURE 9A

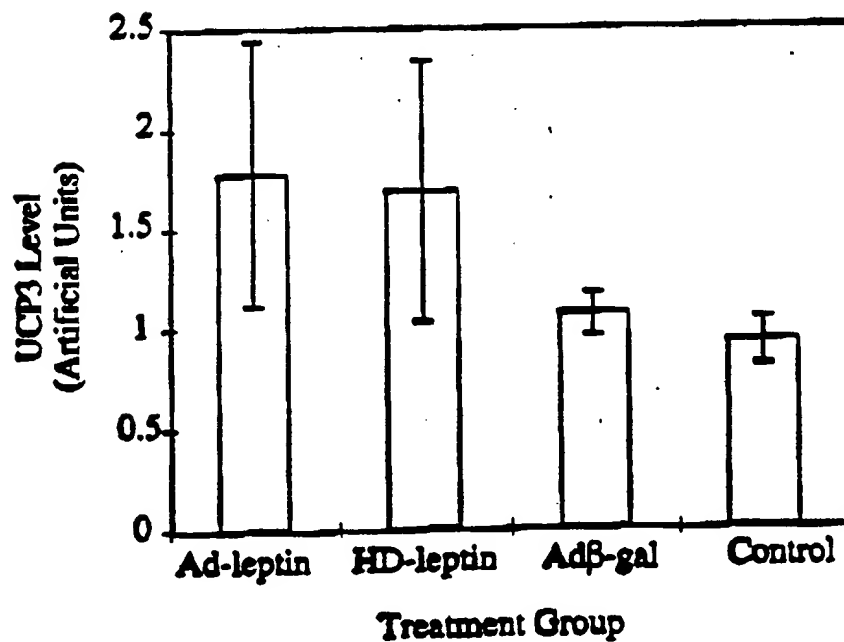


FIGURE 9B